

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Plowman, Gregory
Mossie, Kevin
- (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
AND/OR AUR-2 RELATED DISORDERS
- (iii) NUMBER OF SEQUENCES: 39
- (iv) CORRESPONDENCE ADDRESS:
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Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/012,135
(B) FILING DATE: January 22, 1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/005,268
(B) FILING DATE: January 9, 1998

(A) APPLICATION NUMBER: 08/755,728
 (B) FILING DATE: November 25, 1996

(A) APPLICATION NUMBER: 60/023,943
 (B) FILING DATE: August 14, 1996

(A) APPLICATION NUMBER: 60/008,809
 (B) FILING DATE: December 18, 1995

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1244 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGGAGAGTA | GCAGTGCCTT | GGACCCCAGC | TCTCCTCCCC | CTTTCTCTCT | AAGGATGGCC | 60 |
| CAGAAGGAGA | ACTCCTACCC | CTGGCCCTAC | GGCCGACAGA | CGGCTCCATC | TGGCCTGAGC | 120 |
| ACCCTGCCCC | AGCGAGTCCT | CCGAAAGAG | CCTGTCACCC | CATCTGCACT | TGTCCTCATG | 180 |

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| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|------|
| AGCCGCTCCA | ATGTCCAGCC | CACAGCTGCC | CCTGGCCAGA | AGGTGATGGA | GAATAGCAGT | 240 |
| GGGACACCCG | ACATCTTAAC | GCGGCACTTC | ACAATTGATG | ACTTTGAGAT | TGGGCGTCCT | 300 |
| CTGGGCAAAG | GCAAGTTTGG | AAACGTGTAC | TTGGCTCGGG | AGAAGAAAAG | CCATTTTCATC | 360 |
| GTGGCGCTCA | AGGTCCTCTT | CAAGTCCAG | ATAGAGAAGG | AGGGCGTGGA | GCATCAGCTG | 420 |
| CGCAGAGAGA | TCGAAATCCA | GGCCCACCTG | CACCATCCCA | ACATCCTGCG | TCTCTACAAC | 480 |
| TATTTTTATG | ACCGGAGGAG | GATCTACTTG | ATTCTAGAGT | ATGCCCCCG | CGGGGAGCTC | 540 |
| TACAAGGAGC | TGCAGAAGAG | CTGCACATTT | GACGAGCAGC | GAACAGCCAC | GATCATGGAG | 600 |
| GAGTTGGCAG | ATGCTCTAAT | GTACTGCCAT | GGGAAGAAGG | TGATTACACAG | AGACATAAAG | 660 |
| CCAGAAAATC | TGCTCTTAGG | GCTCAAGGGA | GAGCTGAAGA | TTGCTGACTT | CGGCTGGTCT | 720 |
| GTGCATGCGC | CCTCCCTGAG | GAGGAAGACA | ATGTGTGGCA | CCCTGGACTA | CCTGCCCCCA | 780 |
| GAGATGATTG | AGGGGCGCAT | GCACAATGAG | AAGGTGGATC | TGTGGTGAT | TGGAGTGCTT | 840 |
| TGCTATGAGC | TGCTGCTGGG | GAACCCACCC | TTCGAGAGTG | CATCACACAA | CGAGACCTAT | 900 |
| CGCCGCATCG | TCAAGGTGGA | CCTAAAGTTC | CCCGCTTCTG | TGCCCACGGG | AGCCCAGGAC | 960 |
| CTCATCTCCA | AACTGCTCAG | GCATAACCCC | TCGGAACGGC | TGCCCCTGGC | CCAGGTCTCA | 1020 |
| GCCCACCCTT | GGGTCCGGGC | CAACTCTCGG | AGGGTGCTGC | CTCCCTCTGC | CCTTCAATCT | 1080 |
| GTCGCCTGAT | GGTCCCTGTC | ATTCACCTCG | GTGCGTGTGT | TTGTATGTCT | GTGTATGTAT | 1140 |
| AGGGGAAAGA | AGGGATCCCT | AACTGTTCCC | TTATCTGTTT | TCTACCTCCT | CCTTTGTTTA | 1200 |
| ATAAAGGCTG | AAGCTTTTTG | TAAAAAACA | AAAAAATAA | AAAA | | 1244 |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|-----------------|
| (A) LENGTH: | 2198 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGGATATCTC | AGTGGCGGAC | GAGGACGGCG | GGGACAAGGG | GCGGCTGGTC | GGAGTGGCGG | 60 |
| ACGTCAAGTC | CCCTGTCCGT | TCCTCCGTCC | CTGAGTGTC | TTGGCGCTGC | CTTGTGCCCG | 120 |
| CCCAGCGCCT | TTGCATCCGC | TCCTGGGCAC | CGAGGCGCCC | TGTAGGATAC | TGCTTGTTAC | 180 |
| TTATTACAGC | TAGAGGCATC | ATGGACCGAT | CTAAAGAAAA | CTGCATTTCA | GGACCTGTTA | 240 |
| AGGCTACAGC | TCCAGTTGGA | GGTCCAAAAC | GTGTTCTCGT | GACTCAGCAA | TTTCCTTGTC | 300 |
| AGAATCCATT | ACCTGTAAAT | AGTGGCCAGG | CTCAGCGGGT | CTTGTGTCCT | TCAAATTCTT | 360 |
| CCCAGCGCGT | TCCTTTGCAA | GCACAAAAGC | TTGTCTCCAG | TCACAAGCCG | GTTGAGAATC | 420 |
| AGAAGCAGAA | GCAATTGCAG | GCAACCAAGT | TACCTCATCC | TGTCTCCAGG | CCACTGAATA | 480 |
| ACACCCAAAA | GAGCAAGCAG | CCCCTGCCAT | CGGCACCTGA | AAATAATCCT | GAGGAGGAAC | 540 |
| TGGCATCAAA | ACAGAAAAAT | GAAGAATCAA | AAAAGAGGCA | GTGGGCTTTG | GAAGACTTTG | 600 |
| AAATTGGTCG | CCCTCTGGGT | AAAGGAAAGT | TTGGTAATGT | TTATTGGCA | AGAGAAAAGC | 660 |
| AAAGCAAGTT | TATTCTGGCT | CTTAAAGTGT | TATTTAAAGC | TCAGCTGGAG | AAAGCCGGAG | 720 |
| TGGAGCATCA | GCTCAGAAGA | GAAGTAGAAA | TACAGTCCCA | CCTTCGGCAT | CCTAATATTC | 780 |
| TTAGACTGTA | TGTTATTTTC | CATGATGCTA | CCAGAGTCTA | CCTAATTCTG | GAATATGCAC | 840 |

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|------------|------------|------------|------------|-------------|-------------|------|
| CACTTGGAAC | AGTTTATAGA | GAACCTCAGA | AACTTTCAAA | GTTTGATGAG | CAGAGAACTG | 900 |
| CTACTTATAT | AACAGAATTG | GCAAATGCCC | TGTCTTACTG | TCATTCGAAG | AGAGTTATTC | 960 |
| ATAGAGACAT | TAAGCCAGAG | AACTTACTTC | TTGGATCAGC | TGGAGAGCTT | AAAATTGCAG | 1020 |
| ATTTTGGGTG | GTCAGTACAT | GCTCCATCTT | CCAGGAGGAC | CACTCTCTGT | GGCACCCCTGG | 1080 |
| ACTACCTGCC | CCCTGAAATG | ATTGAAGGTC | GGATGCATGA | TGAGAAGGTG | GATCTCTGGA | 1140 |
| GCCTTGGAGT | TCTTTGCTAT | GAATTTTTAG | TTGGGAAGCC | TCCTTTTGAG | GCAAACACAT | 1200 |
| ACCAAGAGAC | CTACAAAAGA | ATATCACGGG | TTGAATTAC | ATTCCCTGAC | TTTGTAACAG | 1260 |
| AGGGAGCCAG | GGACCTCATT | TCAAGACTGT | TGAAGCATAA | TCCCAGCCAG | AGGCCAATGC | 1320 |
| TCAGAGAAGT | ACTTGAACAC | CCCTGGATCA | CAGCAAATTC | ATCAAAACCA | TCAAATTGCC | 1380 |
| AAAACAAAGA | ATCAGCTAGC | AAACAGTCTT | AGGAATCGTG | CAGGGGGAGA | AATCCTTGAG | 1440 |
| CCAGGGCTGC | CATATAACCT | GACAGGAACA | TGCTACTGAA | GTTTATTTTA | CCATTGACTG | 1500 |
| CTGCCCTCAA | TCTAGAACGC | TACACAAGAA | ATATTTGTTT | TACTCAGCAG | GTGTGCCTTA | 1560 |
| ACCTCCCTAT | TCAGAAAGCT | CCACATCAAT | AAACATGACA | CTCTGAAGTG | AAAGTAGCCA | 1620 |
| CGAGAATTGT | GCTACTTATA | CTGGTTCATA | ATCTGGAGGC | AAGGTTTCGAC | TGCAGCCGCC | 1680 |
| CCGTCAGCCT | GTGCTAGGCA | TGGTGTCTTC | ACAGGAGGCA | AATCCAGAGC | CTGGCTGTGG | 1740 |
| GGAAAGTGAC | CACTCTGCCC | TGACCCCGAT | CAGTTAAGGA | GCTGTGCAAT | AACCTTCCTA | 1800 |
| GTACCTGAGT | GAGTGTGTAA | CTTATTGGGT | TGGCGAAGCC | TGGTAAAGCT | GTTGGAATGA | 1860 |
| GTATGTGATT | CTTTTTAAGT | ATGAAAATAA | AGATATATGT | ACAGACTTGT | ATTTTTTCTC | 1920 |
| TGGTGGCATT | CCTTTAGGAA | TGCTGTGTGT | CTGTCCGGCA | CCCCGGTAGG | CCTGATTGGG | 1980 |
| TTTCTAGTCC | TCCTTAACCA | CTTATCTCCC | ATATGAGAGT | GTGAAAAATA | GGAACACGTG | 2040 |
| CTCTACCTCC | ATTTAGGGAT | TTGCTTGGGA | TACAGAAGAG | GCCATGTGTC | TCAGAGCTGT | 2100 |
| TAAGGGCTTA | TTTTTTTAAA | ACATTGGAGT | CATAGCATGT | GTGTAAACTT | TAAATATGCA | 2160 |
| AATAAATAAG | TATCTATGTC | AAAAAAAAAA | AAAAAAAAA | | | 2198 |

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|-----------------|
| (A) LENGTH: | 344 amino acids |
| (B) TYPE: | amino acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Lys | Glu | Asn | Ser | Tyr | Pro | Trp | Pro | Tyr | Gly | Arg | Gln | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Pro | Ser | Gly | Leu | Ser | Thr | Leu | Pro | Gln | Arg | Val | Leu | Arg | Lys | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |

Pro Val Thr Pro Ser Ala Leu Val Leu Met Ser Arg Ser Asn Val Gln
 35 40 45
 Pro Thr Ala Ala Pro Gly Gln Lys Val Met Glu Asn Ser Ser Gly Thr
 50 55 60
 Pro Asp Ile Leu Thr Arg His Phe Thr Ile Asp Asp Phe Glu Ile Gly
 65 70 75 80
 Arg Pro Leu Gly Lys Gly Lys Phe Gly Asn Val Tyr Leu Ala Arg Glu
 85 90 95
 Lys Lys Ser His Phe Ile Val Ala Leu Lys Val Leu Phe Lys Ser Gln
 100 105 110
 Ile Glu Lys Glu Gly Val Glu His Gln Leu Arg Arg Glu Ile Glu Ile
 115 120 125
 Gln Ala His Leu His His Pro Asn Ile Leu Arg Leu Tyr Asn Tyr Phe
 130 135 140
 Tyr Asp Arg Arg Arg Ile Tyr Leu Ile Leu Glu Tyr Ala Pro Arg Gly
 145 150 155 160
 Glu Leu Tyr Lys Glu Leu Gln Lys Ser Cys Thr Phe Asp Glu Gln Arg
 165 170 175
 Thr Ala Thr Ile Met Glu Glu Leu Ala Asp Ala Leu Met Tyr Cys His
 180 185 190
 Gly Lys Lys Val Ile His Arg Asp Ile Lys Pro Glu Asn Leu Leu Leu
 195 200 205
 Gly Leu Lys Gly Glu Leu Lys Ile Ala Asp Phe Gly Trp Ser Val His
 210 215 220
 Ala Pro Ser Leu Arg Arg Lys Thr Met Cys Gly Thr Leu Asp Tyr Leu
 225 230 235 240
 Pro Pro Glu Met Ile Glu Gly Arg Met His Asn Glu Lys Val Asp Leu
 245 250 255
 Trp Cys Ile Gly Val Leu Cys Tyr Glu Leu Leu Val Gly Asn Pro Pro
 260 265 270
 Phe Glu Ser Ala Ser His Asn Glu Thr Tyr Arg Arg Ile Val Lys Val
 275 280 285
 Asp Leu Lys Phe Pro Ala Ser Val Pro Thr Gly Ala Gln Asp Leu Ile
 290 295 300

Ser Lys Leu Leu Arg His Asn Pro Ser Glu Arg Leu Pro Leu Ala Gln
 305 310 315 320

Val Ser Ala His Pro Trp Val Arg Ala Asn Ser Arg Arg Val Leu Pro
 325 330 335

Pro Ser Ala Leu Gln Ser Val Ala
 340

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro Val Lys Ala Thr
 1 5 10 15

Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln Phe Pro
 20 25 30

Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln Arg Val Leu
 35 40 45

Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln Ala Gln Lys Leu
 50 55 60

Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Gln Leu Gln
 65 70 75 80

Ala Thr Ser Val Pro His Pro Val Ser Arg Pro Leu Asn Asn Thr Gln
 85 90 95

Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu
 100 105 110

Glu Leu Ala Ser Lys Gln Lys Asn Glu Glu Ser Lys Lys Arg Gln Trp
 115 120 125

Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly Lys Gly Lys Phe
 130 135 140

Gly Asn Val Tyr Leu Ala Arg Glu Lys Gln Ser Lys Phe Ile Leu Ala
 145 150 155 160

Leu Lys Val Leu Phe Lys Ala Gln Leu Glu Lys Ala Gly Val Glu His
 165 170 175

Gln Leu Arg Arg Glu Val Glu Ile Gln Ser His Leu Arg His Pro Asn
 180 185 190

Ile Leu Arg Leu Tyr Gly Tyr Phe His Asp Ala Thr Arg Val Tyr Leu
 195 200 205

Ile Leu Glu Tyr Ala Pro Leu Gly Thr Val Tyr Arg Glu Leu Gln Lys
 210 215 220

Leu Ser Lys Phe Asp Glu Gln Arg Thr Ala Thr Tyr Ile Thr Glu Leu
 225 230 235 240

Ala Asn Ala Leu Ser Tyr Cys His Ser Lys Arg Val Ile His Arg Asp
 245 250 255

Ile Lys Pro Glu Asn Leu Leu Leu Gly Ser Ala Gly Glu Leu Lys Ile
 260 265 270

Ala Asp Phe Gly Trp Ser Val His Ala Pro Ser Ser Arg Arg Thr Thr
 275 280 285

Leu Cys Gly Thr Leu Asp Tyr Leu Pro Pro Glu Met Ile Glu Gly Arg
 290 295 300

Met His Asp Glu Lys Val Asp Leu Trp Ser Leu Gly Val Leu Cys Tyr
 305 310 315 320

Glu Phe Leu Val Gly Lys Pro Pro Phe Glu Ala Asn Thr Tyr Gln Glu
 325 330 335

Thr Tyr Lys Arg Ile Ser Arg Val Glu Phe Thr Phe Pro Asp Phe Val
 340 345 350

Thr Glu Gly Ala Arg Asp Leu Ile Ser Arg Leu Leu Lys His Asn Pro
 355 360 365

Ser Gln Arg Pro Met Leu Arg Glu Val Leu Glu His Pro Trp Ile Thr
 370 375 380

Ala Asn Ser Ser Lys Pro Ser Asn Cys Gln Asn Lys Glu Ser Ala Ser
 385 390 395 400

Lys Gln Ser

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Glu Asn Ser Tyr Pro Trp Pro Tyr Gly Arg Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Ile Ser Gly Pro
 1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Gln Phe Pro Gln

1

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Val Asn Ser Gly Gln

1

5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Arg Lys Glu Pro Val Thr Pro Ser Ala Leu Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Met Ser Arg Ser Asn Val Gln Pro Thr Ala Ala Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Val Gln Asn Gln Lys Gln Lys Gln Leu Gln Ala Thr Ser Val Pro His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Pro Val Ser Arg Pro Leu Asn Asn Thr Gln Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Val Met Glu Asn Ser Ser Gly Thr Pro Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ile Leu Thr Arg His Phe Thr Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu Gln
1 5 10 15

Leu Ala Ser Lys Gln Lys
20

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.
The letter "Y" stands for C or T.
The letter "N" stands for A, C, G or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GARTTYGGNG ARGNTNTTYT NGC

23

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "N" stands for A, C, G or T.
 The letter "R" stands for A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AGNACNCCRA ANGCCCACAC RTC

23

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Phe Gly Glu Val Phe Leu Ala
 1 5

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTGGCTCGG GAGAAGAAAA GCCAT
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25

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CAATCATCTC TGGGGGCAGG TAGT

24

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ser Ala Pro Glu Asn Asn Pro Glu Glu Gln Leu Ala Ser Lys
 1 5 10

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(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Arg Pro Leu Asn Asn Thr Gln Lys Ser Lys Gln Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Gln Lys Glu Asn Ser Tyr Pro Trp Pro Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Pro Gly Gln Lys Val Met Glu Asn Ser Ser Gly Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 2, 4, 5 and 7 stands for an unidentified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly Xaa Val
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Val Trp Ser Tyr Phe Gly Ile Val
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 2 and 6 stands
for an unidentified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Xaa Trp Ala Ser Xaa Gly Ile Val
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 4 represents
either Asp or Ser.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Val Trp Xaa Phe Gly Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 21 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CAGGGCAGAG TGGTCACTTT C

21

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 21 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CGTCCGCCAC TCCGACCAGC C

21

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 21 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TGCAGTCGAA CCTTGCCTCC A

21

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 8 amino acids |
| (B) TYPE: | amino acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Asp Val Trp Ala Phe Gly Val Leu
1

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 20 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CGCCTTTGCA TCCGCTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 20 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GATTTCCTC CTGTGAAGAC

20

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 21 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATGCCTCCGG AAAGAGCCTG T

21

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 22 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGTCCCACT GCTATTCTCC AT

22

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 21 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CAGGGCTGCC ATATAACCTG A

21

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

| | |
|-------------------|---------------|
| (A) LENGTH: | 20 base pairs |
| (B) TYPE: | nucleic acid |
| (C) STRANDEDNESS: | single |
| (D) TOPOLOGY: | linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTAGCACAGG CTGACGGGGC

20